



	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	10	
2phk_A																				
1kwp_A	PQTFPLHTSRVLIKEDKERWEDVKDEMISALATRIVDYEQIKIKKTEID										A SNP	LLKKRKRRKKARALEAAALAH									
1jkk_A	DTQQALSSANSHDQFEX																				
21356423.f	MDLEDVNLISLISNM	CHIKPFDVQSPKKNFKDDIYCTYMLD-								VAKPRSTACSEKSGS	FREPTAMPGS	RIVPPIAAPNVTISQVTFALDKS									T PNR D A TS
21356537.f	MELQDAARFPCDLMSSM	CHKRREDVPSKKGDFDDIKYCTYMLLC-							VAKPRSSNSRTKPEAIPVDTLTTPAVSSPLIN	-ITTPVTTIAHVTLALDKN										PPIHS S SAS	
25145948.w	KDQIDEORIEKLICLIFOLIGNKAAIIESVEKKEFEDIHATYLLCERKS								-DESRVSRSATATGASITAGSALAASAANACKHQSSAAASGSSSSRRSSQNDAAATAAGGTVVMSGTRHGGVOMRAQPTSRQATISLLQPPSY	CSSNTTOI											
17562784.w	KDQIDEORIEKLICLIFOLIGNKAAIIESVEKKEFEDIHATYLLCERKS								VAKPRSSNSRTKPEAIPVDTLTTPAVSSPLIN	-ITTPVTTIAHVTLALDKN											
31240093.i	EDLDOKRIPALVAM	CYNRDIEDSANTIMYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
31240095.i	EDLDOKRIPALVAM	CYNRDIEDSANTIMYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
24655791.f	ADLADPKRIPALVAM	CYNRSEIIPASLSQVRYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
24655783.f	ADLADPKRIPALVAM	CYNRSEIIPASLSQVRYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
22726183.i	ADLADPKRIPALVAM	CYNRSEIIPASLSQVRYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
24655778.f	ADLADPKRIPALVAM	CYNRSEIIPASLSQVRYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
24655790.f	ADLADPKRIPALVAM	CYNRSEIIPASLSQVRYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
24655796.f	ADLADPKRIPALVAM	CYNRSEIIPASLSQVRYDDVGATYLLC-							RKSIDDSESDGSRSGSSLSLRNIAGN	EGAAACNSVOOSPTHRGVFSISIASST									KDR SRASSG		
11067437.m	PDYDPDRTEDMVSM	CYTRCEIIDSVPVGGRYNEWATYLLC-							YKSSELEG	DTITLKPRPESADLNN	SSAPSP-SHKVCR-SVSAMP									KDR R SD QA	
MARK2.h	PDYDPDRTEDMVSM	CYTRCEIIDSVPVGGRYNEWATYLLC-							YKSSELEG	DTITLKPRPESADLNN	SSQDFP-SHKVCR-SVSAMP									KDR R SD QA	
6679643.m	LTTOPRIVGVN	LTHTBEIIDSVPVGGRYNEWATYLLC-							YKSSELEG	DTITLKPRPESADLNN	SSQDFP-SHKVCR-SVSAMP									KDR R SD QA	
16758824.m	IDINDAKRIDIMVM	GEARCEINDALVSKYDEVWATYLLC-							RKPPBFEFGESLSSGNCQ	RSPRSSLDNNT	STLQSPAHLKVR-SISANQ									KDR R SD QA	
21704014.m	IDINDAKRIDIMVM	GEARCEINDALVSKYDEVWATYLLC-							RKPPBFEFGESLSSGNCQ	RSPRSSLDNNT	STLQSPAHLKVR-SISANQ									KDR R SD QA	
MARK1.h	IDENDOKRIDIMVM	GEARCEINDALVSKYDEVWATYLLC-							RKPPBFEFGESLSSGNCQ	RSPRSSLDNNT	STLQSPAHLKVR-SISANQ									KDR R SD QA	
12313871.m	IDISDOKRIDIMVM	CYSOEIIQESLSKIKYDEIATYLLC-							RKSABLDASDSSSSSNLSLAKVRNNSDLN	STCOSP-HHKGGF-SVSSSQ										KDR R SD QA	
12313875.m	IDISDOKRIDIMVM	CYSOEIIQESLSKIKYDEIATYLLC-							RKSABLDASDSSSSSNLSLAKVRNNSDLN	STCOSP-HHKGGF-SVSSSQ										KDR R SD QA	
18543359.m	IDISDOKRIDIMVM	CYSOEIIQESLSKIKYDEIATYLLC-							RKSABLDASDSSSSSNLSLAKVRNNSDLN	STCOSP-HHKGGF-SVSSSQ										KDR R SD QA	
MARK3.h	IDISDOKRIDIMVM	CYSOEIIQESLSKIKYDEIATYLLC-							RKSABLDASDSSSSSNLSLAKVRNNSDLN	STCOSP-HHKGGF-SVSSSQ										KDR R SD QA	
34855312.m	EDFCDDKRIBVVMGM	CYTRCEIKEALTNKYNEVATYLLC-							RKTBPBGGDR	GAPCLALARVRAPSDTTNG-TSSKGSSSHNGKGTFTSSSTYH	RDRR R SDFC										
26986591.m	EDFCDDKRIBVVMGM	CYTRCEIKEALTNKYNEVATYLLC-							RKTBPBGGDR	GAPCLALARVRAPSDTTNG-TSSKGSSSHNGKGTFTSSSTYH	RDRR R SDFC										
MARK4.h	EDFDOKRISRVVMGM	LTTRCEIKESTTSKYNEVATYLLC-							RKTBPBGGDR	GAPCLALARVRAPSDTTNG-TSSKGTSHSKGSSSTYH	RDRR R SDFC										
lia8_A	GAKRPRVTSGG	VDESPSG																			
17568289.w	QSTKDNPTIMMFMOHQKWSSEEQIIDAVIQRDFESEIIFATYLLRDKVKKG-								TLECTGEEFRRGSGRSQIDSQKANVDEQLPTPTISAHQADLNLSPPDCDSDDYS										NSDLCDDSP		

	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	12
2phk_A																			
1kwp_A																				
1jkk_A																				
21356423.f	IRPQAPRINAL									KKYICCSAFAKANP	RSPESPSSIPQSAMPKGVGSPVWKTTLLSAORKLAVN									
21356537.f	GRPQAPRINALP									AKPRTTTPARTPARKATNHTSGQGRPEPSLPHPTPSQPKRASAN-MDVK	TILLSAQRLAQAT									
25145948.w	AQIPPLFLRNSTATSSAAQPTSTGITGTRKIADPKGRIPLNSTAVQGHRTATGAVAANNGGIPSHRDHAQQQQYMNQLTSSSTMMSKLINKT									PAAGGTAATSSSSSSATSTAPLQKGSQISHAPTEVIREDDDENSENQONVFLIGGVPQQTSPAVQPTEDATSSSDKE	QQQQKASSETPKESKPSMIHQSPSMPP									
17562784.w	AQIPPLFLRNSTATSSAAQPTSTCITGTRKIADPKGRIPLNSTAVQGHRTATGAVAANNGGIPSHRDHAQQQQYMNQLTSSSTMMSKLINKT									PAAGGTAATSSSSSSATSTAPLQKGSQISHAPTEVIREDDDENSENQONVFLIGGVPQQTSPAVQPTEDATSSSDKE	QQQQKASSETPKESKPSMIHQSPSMPP									
31240093.i	GETR	VG								PTTAVAAAAAAAAVA	SISPPAKRTTSSSTKTDPSNGPTTV-									
31240095.i	GETRKYCVLAGATVNNHS	SGTGSSG								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
24655791.f	AETDRVGP	TNAATVAAATGAVGAVNPNSNNYNAAGSAAADRASVGNSFQKRNTIDS								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
24655783.f	AETDRVGP	TNAATVAAATGAVGAVNPNSNNYNAAGSAAADRASVGNSFQKRNTIDS								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
22726183.i	AETDRVGP	TNAATVAAATGAVGAVNPNSNNYNAAGSAAADRASVGNSFQKRNTIDS								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
24655778.f	AETDRVGP	TNAATVAAATGAVGAVNPNSNNYNAAGSAAADRASVGNSFQKRNTIDS								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
24655800.f	VGTP	TAAATVAAATGAVGAVNPNSNNYNAAGSAAADRASVGNSFQKRNTIDS								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
24655796.f	VGTP	TAAATVAAATGAVGAVNPNSNNYNAAGSAAADRASVGNSFQKRNTIDS								TIKENTARLAACNORPASATKMLTTADT	TIKNSPKAPR-TTNSNGPTTV-									
11067437.m	VPAAPT	TSNSYSK								NKRPPEE	ETGPKASSTAK	VPAASPFLPG	LDRKKTPTPS	SINS						
MARK2.h	GPAAPT	TSNSYSK								NKRPPEE	ETGPKASSTAK	VPAASPFLPG	LDRKKTPTPS	SINS						
6679643.m	VPAAPT	TSNSYSK								NKRPPEE	ETGPKASSTAK	VPAASPFLPG	LDRKKTPTPS	SINS						
16758824.m	GPSIPP	PAVSYTK								RHQANSVES	ECKEEWDKDTA	FRLGSTTIVGS	KSEVTA	SPLVG	PDRKKSAGPENN					
21704014.m	GPAAPT	PAVSYTK								RHQANSVES	ECKEEWDKDTA	FRLGSTTIVGS	KSEVTA	SPLVG	PDRKKSAGPENN					
MARK1.h	GPSIPP	PAVSYTK									ECKEEWDKDTA	FRLGSTTIVGS	KSEVTA	SPLVG	PDRKKSAGPENN					
12313871.m	GPAAPT	SVVAYPK									DKE	DCIPS	FRLGSSS	VGG	KGIA	PA	MLGNAGN	PKADIP	PRKKS	PSP
12313875.m	GPAAPT	SVVAYPK									DKE	DCIPS	FRLGSSS	VGG	KGIA	PA	MLGNAGN	PKADIP	PRKKS	PSP
18543359.m	GPAAPT	SVVAYPK									DKE	DCVIPS	FRLGSSS	VGG	KGIA	PA	MLGNAGN	PKADIP	PRKKS	PSP
MARK3.h	GPAAPT	SVVAYPK									DKE	DCVIPS	FRLGSSS	VGG	KGIA	PA	MLGNAGN	PKADIP	PRKKS	PSP
34855312.m	GPAAPT	SPALHPK									EKE	ERLPCKPKACSAAGSGSRGLPPSPMVSAHNPKAIEP	PRKKS	STP	NN					
26986591.m	GPAAPT	SPALHPK									EKE	ERLPCKPKACSAAGSGSRGLPPSPMVSAHNPKAIEP	PRKKS	STP	NN					
MARK4.h	GPAAPT	SPALHPK									EKE	ERLPCKPKACSAAGSGSRGLPPSPMVSAHNPKAIEP	PRKKS	STP	NN					
lia8_A																				
17568289.w	MSSMGPMPNHERQFTGTPHGLDII	GNRFENRRHTLCASEQLLSFNMMGQFPNNLLNN								FSMNPPLGFPPMPFEGQA	EFPLPSLHFA	TIPIDL	SKMLPV	PKSFERRASAGET	LLPTN					

Sequence logo showing the conservation of amino acids at each position of the alignment. The x-axis represents positions 1410 to 1570. The y-axis lists protein names. Each position has a stack of four bars representing the frequency of A, T, C, and G. A color scale from green (highest) to red (lowest) indicates the probability of each nucleotide at that position.